1634

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RAW SEQUENCE LISTING
PATENT APPLICATION   *US/08/939,905*

DATE: 05/26/98
TIME: 09:47:17

INPUT SET: S26075.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

SEQUENCE LISTING   ENTE

1
2
3   (1)   General Information:
4
5   (i) APPLICANT: GIJZEN, Mark
6
7   (ii) TITLE OF INVENTION:SEED COAT SPECIFIC DNA REGULATORY REGION
8   AND PEROXIDASE
9
10   (iii) NUMBER OF SEQUENCES: 2
11
12   (iv) CORRESPONDENCE ADDRESS:
13   (A) ADDRESSEE: NIXON & VANDERHYE P.C.
14   (B) STREET: 8th Floor, 1100 North Glebe Road
15   (C) CITY: Arlington
16   (D) STATE: Virginia
17   (E) COUNTRY: United States
18   (F) ZIP: 22201-4714
19
20   (v) COMPUTER READABLE FORM:
21   (A) MEDIUM TYPE: Floppy disk
22   (B) COMPUTER: IBM PC compatible
23   (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24   (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
25
26   (vi) CURRENT APPLICATION DATA:
27   (A) APPLICATION NUMBER:
28   (B) FILING DATE: 26-SEP-1997
29   (C) CLASSIFICATION:
30
31   (vii) PRIOR APPLICATION DATA:
32   (A) APPLICATION NUMBER: US 08/723,414
33   (B) FILING DATE: 30-SEP-1996
34
35   (viii) ATTORNEY/AGENT INFORMATION:
36   (A) NAME: BYRNE, Thomas E.
37   (B) REGISTRATION NUMBER: 32,205
38   (C) REFERENCE/DOCKET NUMBER: 76-105
39
40   (ix) TELECOMMUNICATION INFORMATION:
41   (A) TELEPHONE: (703) 816-4021
42   (B) TELEFAX: (703) 816-4100
43
44
45   (2) INFORMATION FOR SEQ ID NO: 1:
46

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RAW SEQUENCE LISTING
PATENT APPLICATION   *US/08/939,905*

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47          (i) SEQUENCE CHARACTERISTICS:
48              (A) LENGTH: 1244 base pairs
49              (B) TYPE: nucleic acid
50              (C) STRANDEDNESS: single
51              (D) TOPOLOGY: linear
52
53
54      (ii) MOLECULE TYPE: cDNA
55
56      (iii) HYPOTHETICAL: NO
57
58      (iv) ANTI-SENSE: NO
59
60
61      (ix) FEATURE:
62              (A) NAME/KEY: CDS
63              (B) LOCATION:1..1056
64
65      (ix) FEATURE:
66              (A) NAME/KEY: sig_peptide
67              (B) LOCATION:1..77
68
69
70      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
71
72      ATG GGT TCC ATG CGT CTA TTA GTA GTG GCA TTG TTG TGT GCA TTT GCT     48
73      Met Gly Ser Met Arg Leu Leu Val Val Ala Leu Leu Cys Ala Phe Ala
74       1               5                  10                  15
75
76      ATG CAT GCA GGT TTT TCA GTC TCT TAT GCT CAG CTT ACT CCT ACG TTC     96
77      Met His Ala Gly Phe Ser Val Ser Tyr Ala Gln Leu Thr Pro Thr Phe
78                       20                  25                  30
79
80      TAC AGA GAA ACA TGT CCA AAT CTG TTC CCT ATT GTG TTT GGA GTA ATC    144
81      Tyr Arg Glu Thr Cys Pro Asn Leu Phe Pro Ile Val Phe Gly Val Ile
82                   35                  40                  45
83
84      TTC GAT GCT TCT TTC ACC GAT CCC CGA ATC GGG GCC AGT CTC ATG AGG    192
85      Phe Asp Ala Ser Phe Thr Asp Pro Arg Ile Gly Ala Ser Leu Met Arg
86           50                  55                  60
87
88      CTT CAT TTT CAT GAT TGC TTT GTT CAA GGT TGT GAT GGA TCA GTT TTG    240
89      Leu His Phe His Asp Cys Phe Val Gln Gly Cys Asp Gly Ser Val Leu
90       65                  70                  75                  80
91
92      CTG AAC AAC ACT GAT ACA ATA GAA AGC GAG CAA GAT GCA CTT CCA AAT    288
93      Leu Asn Asn Thr Asp Thr Ile Glu Ser Glu Gln Asp Ala Leu Pro Asn
94                   85                  90                  95
95
96      ATC AAC TCA ATA AGA GGA TTG GAC GTT GTC AAT GAC ATC AAG ACA GCG    336
97      Ile Asn Ser Ile Arg Gly Leu Asp Val Val Asn Asp Ile Lys Thr Ala
98                   100                 105                 110
99
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/939,905*

INPUT SET: S26075.raw

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101   Val Glu Asn Ser Cys Pro Asp Thr Val Ser Cys Ala Asp Ile Leu Ala
102           115                 120                 125

103
104   ATT GCA GCT GAA ATA GCT TCT GTT CTG GGA GGA GGT CCA GGA TGG CCA      432
105   Ile Ala Ala Glu Ile Ala Ser Val Leu Gly Gly Gly Pro Gly Trp Pro
106           130                 135                 140

107
108   GTT CCA TTA GGA AGA AGG GAC AGC TTA ACA GCA AAC CGA ACC CTT GCA      480
109   Val Pro Leu Gly Arg Arg Asp Ser Leu Thr Ala Asn Arg Thr Leu Ala
110   145                 150                 155                 160

111
112   AAT CAA AAC CTT CCA GCA CCT TTC TTC AAC CTC ACT CAA CTT AAA GCT      528
113   Asn Gln Asn Leu Pro Ala Pro Phe Phe Asn Leu Thr Gln Leu Lys Ala
114                       165                 170                 175

115
116   TCC TTT GCT GTT CAA GGT CTC AAC ACC CTT GAT TTA GTT ACA CTC TCA      576
117   Ser Phe Ala Val Gln Gly Leu Asn Thr Leu Asp Leu Val Thr Leu Ser
118                       180                 185                 190

119
120   GGT GGT CAT ACG TTT GGA AGA GCT CGG TGC AGT ACA TTC ATA AAC CGA      624
121   Gly Gly His Thr Phe Gly Arg Ala Arg Cys Ser Thr Phe Ile Asn Arg
122           195                 200                 205

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124   TTA TAC AAC TTC AGC AAC ACT GGA AAC CCT GAT CCA ACT CTG AAC ACA      672
125   Leu Tyr Asn Phe Ser Asn Thr Gly Asn Pro Asp Pro Thr Leu Asn Thr
126           210                 215                 220

127
128   ACA TAC TTA GAA GTA TTG CGT GCA AGA TGC CCC CAG AAT GCA ACT GGG      720
129   Thr Tyr Leu Glu Val Leu Arg Ala Arg Cys Pro Gln Asn Ala Thr Gly
130   225                 230                 235                 240

131
132   GAT AAC CTC ACC AAT TTG GAC CTG AGC ACA CCT GAT CAA TTT GAC AAC      768
133   Asp Asn Leu Thr Asn Leu Asp Leu Ser Thr Pro Asp Gln Phe Asp Asn
134                       245                 250                 255

135
136   AGA TAC TAC TCC AAT CTT CTG CAG CTC AAT GGC TTA CTT CAG AGT GAC      816
137   Arg Tyr Tyr Ser Asn Leu Leu Gln Leu Asn Gly Leu Leu Gln Ser Asp
138                       260                 265                 270

139
140   CAA GAA CTT TTC TCC ACT CCT GGT GCT GAT ACC ATT CCC ATT GTC AAT      864
141   Gln Glu Leu Phe Ser Thr Pro Gly Ala Asp Thr Ile Pro Ile Val Asn
142           275                 280                 285

143
144   AGC TTC AGC AGT AAC CAG AAT ACT TTC TTT TCC AAC TTT AGA GTT TCA      912
145   Ser Phe Ser Ser Asn Gln Asn Thr Phe Phe Ser Asn Phe Arg Val Ser
146           290                 295                 300

147
148   ATG ATA AAA ATG GGT AAT ATT GGA GTG CTG ACT GGG GAT GAA GGA GAA      960
149   Met Ile Lys Met Gly Asn Ile Gly Val Leu Thr Gly Asp Glu Gly Glu
150   305                 310                 315                 320

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152   ATT CGC TTG CAA TGT AAT TTT GTG AAT GGA GAC TCG TTT GGA TTA GCT     1008
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153   Ile Arg Leu Gln Cys Asn Phe Val Asn Gly Asp Ser Phe Gly Leu Ala
154                   325             330             335
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156   AGT GTG GCG TCC AAA GAT GCT AAA CAA AAG CTT GTT GCT CAA TCT AAA      1056
157   Ser Val Ala Ser Lys Asp Ala Lys Gln Lys Leu Val Ala Gln Ser Lys
158                   340             345             350
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160   TAAACCAATA ATTAATGGGG ATGTGCATGC TAGCTAGCAT GTAAAGGCAA ATTAGGTTGT    1116
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162   AAACCTCTTT GCTAGCTATA TTGAAATAAA CCAAAGGAGT AGTGTGCATG TCAATTCGAT    1176
163
164   TTTGCCATGT ACCTCTTGGA ATATTATGTA ATAATTATTT GAATCTCTTT AAGGTACTTA    1236
165                                                                       1244
166   ATTAATCA
167
168
169
170   (2) INFORMATION FOR SEQ ID NO: 2:
171
172       (i) SEQUENCE CHARACTERISTICS:
173           (A) LENGTH: 4700 base pairs
174           (B) TYPE: nucleic acid
175           (C) STRANDEDNESS: single
176           (D) TOPOLOGY: linear
177
178      (ii) MOLECULE TYPE: DNA (genomic)
179
180
181      (ix) FEATURE:
182           (A) NAME/KEY: promoter
183           (B) LOCATION:1..1532
184
185      (ix) FEATURE:
186           (A) NAME/KEY: sig_peptide
187           (B) LOCATION:1533..1609
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189      (ix) FEATURE:
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191           (B) LOCATION:1533..1751
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195           (B) LOCATION:2383..2574
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203           (B) LOCATION:4033..4516
204
205      (ix) FEATURE:
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206              (A) NAME/KEY: intron
207              (B) LOCATION:1752..1782
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209     (ix) FEATURE:
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211              (B) LOCATION:2575..3604
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213     (ix) FEATURE:
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215              (B) LOCATION:3770..4032
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217     (ix) FEATURE:
218              (A) NAME/KEY: CDS
219              (B) LOCATION:1533..1751
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221     (ix) FEATURE:
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223              (B) LOCATION:2383..2574
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225     (ix) FEATURE:
226              (A) NAME/KEY: CDS
227              (B) LOCATION:3605..3769
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229     (ix) FEATURE:
230              (A) NAME/KEY: CDS
231              (B) LOCATION:4033..4516
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233
234     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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236  TAGATAAAAA AATGGGATAT AATTTTTCTC AGATGTTGTT TATACTGTTT TTTTAATCAG      60
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238  AATTAAAATT CCTCTTTAAT TATCGACATA ATTTTTTTTG GTGAATATTA TCGACATAAT     120
239
240  TATTTAATAC AAATTTTTAT TGTACATAGA AGTGATACTT CAATTTTAAT ATTGGAGAAC     180
241
242  AGTACGAAAA CATAAAAAAA CTGTTATTAG AAGAAAAAAA TATATGGAAA AGGTTAGCTA     240
243
244  CATATATTAG CTAAATTAGT TGTTCTAATT GGCTATATAA ACCCTATTGT ACTCTTTGTA     300
245
246  ATCTCACCTT TTTCATTTAA ATACATTTCT ACTTTTTAAG TTCTATATTT TCTCTCAATT     360
247
248  TTCTTCGATA AACCATGAAA TTTAACATGG TATATCAGCG ATACCACCCA CTTTGAAAGC     420
249
250  CATGTATGGC TAGTATGGGC AGCCAAAATT TGCCCTGGTT CAAGCAAAGC AAGTGTTTAT     480
251
252  ATAGATGTGA CTTTTGTTGA GGAACTCATG CCAATGGTAC TGATTGTGAA ACTGAGAAAA     540
253
254  CTAATTTGGA GAATTTGAAT TATGATCATT AAATACTCCT CTCCTGACTA CCTTCGTCCC     600
255
256  TCAAATTTGT ACCATCATTA TTTCCCAAAA ATTTGATTAC AATGCACTAA TTAATGAATG     660
257
258  TTTCTTACAT TATCATATTA TCATATCTGA CATTTTGTTT TTACTTTTTA TAATAATTAT     720
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/08/939,905*

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